

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 09/763,957A

Source: 1FW16

Date Processed by STIC: 3/14/05

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IFW16

RAW SEQUENCE LISTING

DATE: 03/14/2005

PATENT APPLICATION: US/09/763,957A

TIME: 11:01:17

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Output Set: N:\CRF4\03142005\I763957A.raw

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3 <110> APPLICANT: Mesa, Jose Ramon Botella
4   Cazzonelli, Christopher Ian
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8 <130> FILE REFERENCE: 229752001300
10 <140> CURRENT APPLICATION NUMBER: 09/763,957A
11 <141> CURRENT FILING DATE: 2001-06-18
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15 <170> SOFTWARE: PatentIn Ver. 2.0
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20 <211> LENGTH: 1923
22 <212> TYPE: DNA
24 <213> ORGANISM: Plant
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40                               Met Gly Phe Lys Ala Met Asp Gln Thr
42                               1           5
44 ccc ttg ttg tcc aag atg gct att ggg gat gga cat ggc gaa tca tcc 162
46 Pro Leu Leu Ser Lys Met Ala Ile Gly Asp Gly His Gly Glu Ser Ser
48 10           15           20           25
52 cca tac ttt gat gga tgg aag gct tat gat caa aac ccc ttt cat ccc 210
54 Pro Tyr Phe Asp Gly Trp Lys Ala Tyr Asp Gln Asn Pro Phe His Pro
56           30           35           40
60 aca gat aat cct aac ggt gtt atg caa atg ggt ctt gct gag aat cag 258
62 Thr Asp Asn Pro Asn Gly Val Met Gln Met Gly Leu Ala Glu Asn Gln
64           45           50           55
68 ctt acc tct gat ttg gtt gaa gat tgg ata ctg aac aac cct gaa gcc 306
70 Leu Thr Ser Asp Leu Val Glu Asp Trp Ile Leu Asn Asn Pro Glu Ala
72           60           65           70
76 tcc att tgc act cca gaa gga ata aat gat ttc agg gcc ata gct aac 354
78 Ser Ile Cys Thr Pro Glu Gly Ile Asn Asp Phe Arg Ala Ile Ala Asn
80           75           80           85
84 ttt cag gat tat cat ggt ctg gcc gag ttc aga aat gct gtg gct aaa 402
86 Phe Gln Asp Tyr His Gly Leu Ala Glu Phe Arg Asn Ala Val Ala Lys
88 90           95           100          105
92 ttt atg gct aga aca agg gga aac aga atc acg ttt gac cct gac cgt 450
94 Phe Met Ala Arg Thr Arg Gly Asn Arg Ile Thr Phe Asp Pro Asp Arg
96           110          115          120
100 att gtc atg agc ggt gga gcc acc gga gca cac gaa gtc act gcc ttt 498
102 Ile Val Met Ser Gly Gly Ala Thr Gly Ala His Glu Val Thr Ala Phe

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104		125		130		135		
108	tgt	ttg	gca	gat	ccc	ggc	gag	gca
110	Cys	Leu	Ala	Asp	Pro	Gly	Glu	Ala
112			140			145		150
116	cca	ggc	ttt	gac	cgg	gat	ttg	agg
118	Pro	Gly	Phe	Asp	Arg	Asp	Leu	Arg
120		155				160		165
124	cca	ggt	atg	tgc	gat	agc	tca	aat
126	Pro	Val	Met	Cys	Asp	Ser	Ser	Asn
128	170					175		180
132	ttg	gaa	gat	gcc	tat	gag	aaa	gca
134	Leu	Glu	Asp	Ala	Tyr	Glu	Lys	Ala
136				190				195
140	ggt	tta	ctg	atc	acc	aat	cca	tca
142	Gly	Leu	Leu	Ile	Thr	Asn	Pro	Ser
144			205				210	
148	aga	aag	aca	ctg	aga	acc	gtg	gtg
150	Arg	Lys	Thr	Leu	Arg	Thr	Val	Val
152		220					225	
156	cac	ctt	gta	tgt	gat	gaa	ata	tat
158	His	Leu	Val	Cys	Asp	Glu	Ile	Tyr
160		235				240		245
164	ggt	ttc	ata	agc	ata	gct	gag	ata
166	Gly	Phe	Ile	Ser	Ile	Ala	Glu	Ile
168	250					255		260
172	tgt	gac	cgc	aac	ctc	gta	cac	att
174	Cys	Asp	Arg	Asn	Leu	Val	His	Ile
176				270				275
180	ggg	ttc	cct	ggc	ttc	aga	gtc	ggc
182	Gly	Phe	Pro	Gly	Phe	Arg	Val	Gly
184				285				290
188	gtg	ggt	aat	tgt	gca	cgc	aaa	atg
190	Val	Val	Asn	Cys	Ala	Arg	Lys	Met
192		300					305	
196	cag	act	cag	tat	ctt	tta	gca	tcg
198	Gln	Thr	Gln	Tyr	Leu	Leu	Ala	Ser
200		315					320	
204	gag	agg	ttt	ctg	gca	gag	agc	gca
206	Glu	Arg	Phe	Leu	Ala	Glu	Ser	Ala
208	330					335		340
212	ggt	ttc	act	ggg	ggg	ttg	gcc	aaa
214	Val	Phe	Thr	Gly	Gly	Leu	Ala	Lys
216				350				355
220	aat	gct	ggt	cta	ttt	gtg	tgg	atg
222	Asn	Ala	Gly	Leu	Phe	Val	Trp	Met
224				365				370
228	cca	act	ttc	gac	tct	gaa	acg	gag
230	Pro	Thr	Phe	Asp	Ser	Glu	Thr	Glu
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236 gtt aag atc aat gtt tca cct ggc tat tcc ttc cat tgc act gag cca 1314
238 Val Lys Ile Asn Val Ser Pro Gly Tyr Ser Phe His Cys Thr Glu Pro
240 395 400 405
244 ggg tgg ttt agg gtg tgc tat gcc aac atg gat atg gct gtg caa 1362
246 Gly Trp Phe Arg Val Cys Tyr Ala Asn Met Asp Asp Met Ala Val Gln
248 410 415 420 425
252 att gct ttg caa cga atc cgc aac ttt gtg ctt caa aac aag gag gtc 1410
254 Ile Ala Leu Gln Arg Ile Arg Asn Phe Val Leu Gln Asn Lys Glu Val
256 430 435 440
260 gtg gtg tct aat aag aaa cat tgt tgg cac agt aac ttg agg ctg agc 1458
262 Val Val Ser Asn Lys Lys His Cys Trp His Ser Asn Leu Arg Leu Ser
264 445 450 455
268 ctc aaa acc aga agg ttt gat gat atc acc atg tca cct cac tct ccc 1506
270 Leu Lys Thr Arg Arg Phe Asp Asp Ile Thr Met Ser Pro His Ser Pro
272 460 465 470
276 cta cct cag tca cct atg gtt aaa gcc aca aat tgagtttgca tattcctctg 1559
278 Leu Pro Gln Ser Pro Met Val Lys Ala Thr Asn
280 475 480
284 aatcgtttag aagaagtaac tgatatgtga agattacttg gttcttttat ttgttatttt 1619
288 gagaaggtac ataagtgtctg gatttggttct ttggaacagc aataacagga aattcctgat 1679
292 gttgttttgt gatcggtatc acaatccagt gtctacaag ttgtgctgct tcatgcacgc 1739
296 cccctcaatc ttagggtcat tttttctttt ttcacttacc aaagggtcaa ggtgaaaaaa 1799
300 gtttatagag tctgtaattgt tattgggttta tcagaagagt ccaaaagatg tctgtaattct 1859
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308 ttcc 1923
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316 <211> LENGTH: 484
318 <212> TYPE: PRT
320 <213> ORGANISM: Plant
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332 20 25 30
335 Ala Tyr Asp Gln Asn Pro Phe His Pro Thr Asp Asn Pro Asn Gly Val
337 35 40 45
341 Met Gln Met Gly Leu Ala Glu Asn Gln Leu Thr Ser Asp Leu Val Glu
343 50 55 60
347 Asp Trp Ile Leu Asn Asn Pro Glu Ala Ser Ile Cys Thr Pro Glu Gly
349 65 70 75 80
353 Ile Asn Asp Phe Arg Ala Ile Ala Asn Phe Gln Asp Tyr His Gly Leu
355 85 90 95
359 Ala Glu Phe Arg Asn Ala Val Ala Lys Phe Met Ala Arg Thr Arg Gly
361 100 105 110
365 Asn Arg Ile Thr Phe Asp Pro Asp Arg Ile Val Met Ser Gly Gly Ala
367 115 120 125
371 Thr Gly Ala His Glu Val Thr Ala Phe Cys Leu Ala Asp Pro Gly Glu
373 130 135 140
377 Ala Phe Leu Val Pro Ile Pro Tyr Tyr Pro Gly Phe Asp Arg Asp Leu

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391          180          185          190
395 Ala Arg Glu Asp Asn Ile Arg Val Lys Gly Leu Leu Ile Thr Asn Pro
397          195          200          205
401 Ser Asn Pro Leu Gly Thr Ile Met Asp Arg Lys Thr Leu Arg Thr Val
403          210          215          220
407 Val Ser Phe Ile Asn Glu Lys Arg Ile His Leu Val Cys Asp Glu Ile
409 225          230          235          240
413 Tyr Ala Ala Thr Val Phe Ser Gln Pro Gly Phe Ile Ser Ile Ala Glu
415          245          250          255
419 Ile Leu Glu Asp Glu Thr Asp Ile Glu Cys Asp Arg Asn Leu Val His
421          260          265          270
425 Ile Val Tyr Ser Leu Ser Lys Asp Met Gly Phe Pro Gly Phe Arg Val
427          275          280          285
431 Gly Ile Ile Tyr Ser Tyr Asn Asp Ala Val Val Asn Cys Ala Arg Lys
433          290          295          300
437 Met Ser Ser Phe Gly Leu Val Ser Thr Gln Thr Gln Tyr Leu Leu Ala
439 305          310          315          320
443 Ser Met Leu Asn Asp Glu Phe Val Glu Arg Phe Leu Ala Glu Ser
445          325          330          335
449 Ala Lys Arg Leu Ala Gln Arg Phe Arg Val Phe Thr Gly Gly Leu Ala
451          340          345          350
455 Lys Val Gly Ile Lys Cys Leu Gln Ser Asn Ala Gly Leu Phe Val Trp
457          355          360          365
461 Met Asp Leu Arg Gln Leu Leu Lys Lys Pro Thr Phe Asp Ser Glu Thr
463          370          375          380
467 Glu Leu Trp Lys Val Ile Ile His Glu Val Lys Ile Asn Val Ser Pro
469 385          390          395          400
473 Gly Tyr Ser Phe His Cys Thr Glu Pro Gly Trp Phe Arg Val Cys Tyr
475          405          410          415
479 Ala Asn Met Asp Asp Met Ala Val Gln Ile Ala Leu Gln Arg Ile Arg
481          420          425          430
485 Asn Phe Val Leu Gln Asn Lys Glu Val Val Val Ser Asn Lys Lys His
487          435          440          445
491 Cys Trp His Ser Asn Leu Arg Leu Ser Leu Lys Thr Arg Arg Phe Asp
493          450          455          460
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539 tatttgtagg cgtattcatt tctcctttcc tacaataatc cttgggtgct ctttatcgga 300
543 aaaaaaccaa aagcaatagc tactctgtaa ggtcctcgat tgccgacaag aacatcacat 360
547 gcgtgctgtc gaagaacaca taattttgag gttgaagctc acgtgcgagt tttgcatatt 420
551 tttaggttat gtgtacacgt atggagtgag ttccgcgat atagtgtagg tagttgagtg 480
555 gctgagtagc gagtgaatca ggtaacacta tcttttcaag ccacctaat aagggattta 540
559 atgttcatgc aactgttctt cgctaactaa ggccccactt acctttataa tattctctct 600
563 aactccgggc ttttggttaag tacaactttt ctactcttat ttaatggagg gattattttt 660
567 tccatatacc aattaattta ttttttaatt tatgcatttt gatcttatat taaaacaatt 720
571 atggtatgga ttaagtcgta tatcggtgac aattgaagtt ttctcgaag ttagccattt 780
575 ttatgaaatt aaacttaatc actactatta ggtaaattca tatgtatcat taacaatttc 840
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583 tgtattataa ggttgacgac tttaacctaa atctattttg aattgaaggg gttgatgact 960
587 tcagctttta aataattcaa cttaaagttct agactacatt ggagatttta gtgttcataa 1020
591 aatttttaga aaaggctgag ttaaagttat gaaaaagatt ggtgactatt caattaatta 1080
595 gttgtgaatt gatgacaaat atttcatgag cataaccaat cagagaaata ccacctcgac 1140
599 cgactacaac aatctcaatg ttaattaatg aagcattgta gtataaggag tctagaataa 1200
603 atttctttaa tattagagga aaactatttt taaaaaatta caagaaaagt ttgatctata 1260
607 acctctttta actttaaatt atctaacaat tttcttatga ctacattgt gttgataggg 1320
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615 agtattaact tggagaaatg attgcctaag aagttataaa aaaggagaaa atatttattc 1440
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623 taatttaata agtattgaat gtagaataat ttttatttat aaatttgaac taaaatattc 1560
627 aaataatatt caaagtaaat aatagatata attcatcatt caatacgagt aattcaatct 1620
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635 ctaaatata attaatttct ttgaatatct tttatacaag taggtagact agaagaatta 1740
639 tcttatctcc cgtatatttg tagatgttaa atgtaacggg cttagactga tgtttttgta 1800
643 ttatattatt tataaatcca ttagagattt aagttaatgt ctctctttga ttttaacatg 1860
647 gttctaaaaa ttaggtttta tcattgcgtc ctcaatgaac ccattgctata tgttttaag 1920
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655 ttgatactag aaaacgaaga agtagagagt agtgatatca cgtgtaaaaa ataatagttg 2040
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671 cttcttctc tggaaacttc atcgatgtgg acttctgtct ctcaaaagtc aagctcaatt 2280
675 tatccaatgc attataaata cacactctcc ctcccttcta ttcttcattg catcacattt 2340
679 cctctataaa ttactcacac cttattccta acttcatttc aacatcctct ctcccactta 2400
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695 <211> LENGTH: 29
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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 03/14/2005
PATENT APPLICATION: US/09/763,957A TIME: 11:01:18

Input Set : D:\229752001300.txt
Output Set : N:\CRF4\03142005\I763957A.raw

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The rules require that a line not exceed 72 characters in length. This includes spaces.

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